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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant:

Robert A. Murgita

Art Unit:

1647

Serial No.:

08/879,469

Examiner:

Stephen Gucker

Filed:

June 20, 1997

Customer No.:

21559

Title:

RECOMBINANT HUMAN ALPHA-FETOPROTEIN AS A CELL

PROLIFERATIVE AGENT

Mail Stop Petition Commissioner for Patents P.O. Box 1450 Alexandria, VA 22313-1450

TRANSMITTAL OF FORMAL DRAWINGS TO OFFICIAL DRAFTSPERSON

In reply to the Notice of Allowability that was mailed in connection with the above-captioned case on March 21, 2003, and with reference to the Notice of Allowance that was mailed on March 21, 2003, having confirmation number 9547, enclosed are:

Five sheets of formal drawings that replace the informal drawings filed with the application include the changes required by the Official Draftsperson.

If there are any other charges or any credits, please apply them to Deposit Account No.

03-2095.

-1. W

Respectfully submitted,

Date: 28 July 2004

TODO ARMSTRONG, Ph.D. REG. NO. 54, 590

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			;	1 /5)	
			:	1/5				
	181 GAA	151 his CAT	121 gln CAA	91 his CAT		31 Phe TTT	ATTO	
	roc rocys	333 ord	val GTT	ser	glu gaa	phe	leu CTG	
	phe	phe TTC	pro	asp GAC		ala	his	
	gln	leu CTG	glu GAA	cys TGC	ser	gln CAG	arg	
	thr	tyr :	pro	cys TGC	ser TCA	phe TTT	asn AAT	1
	lys	ala GCA	pro val	ser	ser gly cys TCA GGG TGT	phe val	glu GAA	TO THE CONTROL OF THE
		pro	thr ACA	gln	cys	gln CAA	tyr TAT	HACA.
	190 ala ala thr val GCA GCA ACA GTT	thr	ser AGC	ser AGT	leu TTA	glu GAA	10 r gly ile ala : r GGA ATA GCT :	NAAT.
	thr	ile	cys TGT	glu GAA	glu	ala GCC	ile ATA	NACT.
	190 r val 'A GTT	160 leu CTT	130 glu GAA	100 glu GAG	70 asn AAC	40 thr ACT	10 ala GCT	AGCA
	thr	leu CTT	ala GCA	gly GGA	gln CAG	tyr TAC		
	lys MAA	Tog Qui	tyr TAT	arg	leu CTA		ile ATA	-19 met
	glu	trp ala	glu GAA	his CAT	L)	glu GAA	leu TTG	-19 met lys ATG AAG
į	lys glu leu AAA GAA TTA	ala GCT	glu GAA	asn AAC	ala GCC	val GTA	asp GAT	13 CT
_ _	lys glu leu arg glu ser ser AAA GAA TTA AGA GAA AGC AGC	erg	asp	his asn cys	phe	lys glu val ser lys met val AAG GAA GTA AGC AAA ATG GTG	ile leu asp ser	p val glu ser ile I G GTG GAA TCA ATT (
	arg glu ser ser AGA GAA AGC AGC	tyr Tai	arg AGG	s phe leu o	leu glu CTG GAA	lys AAA	tyr TAC	glu GAA
	Ser	asp GAC	glu GAG	leu CTT	glu GAA	met ATG	gln	ser
	ser AGC	lys AAA	thr	ala GCA	glu GAA	val GTG	cys TCT	ile ATT
	200 leu leu mrG mmA	ile ATA	phe	his cac	leu CTT	lys asp AAA GAT	ACT	phe leu
	200 leu TTA	170 ile ATT	140 met ATG	lys lys	80 TGC	asp GAT	-	leu :
	asn MT	bro pro	asn lys ph	lys AAG (his car	ala GCA	glu :	-10 ile ATT
	gln	rer .	lys :	000 ord	glu GAG	leu	ATA	Phe :
	n gln his a	S S	9 D	thr	lys AAA	ACT	AGT) e phe leu leu r rrc cra cra
	ala (GCA	recys :	ile tyr ATT TAT	CCA o	glu GAA	ala GCA	leu a	TAN A
	ala cys ala val met GCA TGT GCA GTA ATG	lys a	tyr (ala :	ile leu glu Arr TTG GAG	ile glu lys ATT GAG AAA	ala : GCT (asn I
	ala . GCA	ala :	glu ile ala GAG ATA GCA	ser ile	leu :	glu GAG	asp :	phe t
	val GTA	glu GAA	ile a	ATC (glu GAG	lys :	CTG O	ACT C
	met ATG	asn AAT	ala GCA	CCA ord	lys AAG	Dro pro	u ala asp leu ala A GCT GAC CTG GCT	glu ser
	lys	ala : GCA :	arg AGA	leu CTT	tyr TAC	ACT	Acc	LCC Ser
	210 asn AAT	180 val GTT	arg AGG	Phe Ph	gly GGA	gly GGA	ile ATA	AT -1 arg AGA =

Fig. 1A

(731)

(641)

(551)

(461)

(371)

(2)



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421 pro CCC	391 ala GCA	361 leu TTA	331 phe TTC	301 asp GAT	271 ser TCT	241 leu CTG	211 phe
gln	leu	leu	leu	glu	gln	asp	gly
CAG	TTG	TTG	TTG	GAA	CAA	GAT	
leu	ala	glu	ala	lys	gln	val	Acc
CTG	GCA	GAG	GCA	AAA	CAA	CTG	
thr Acc	lys AAG	lys AAG	ser	133 ord	asp	ala GCC	arg
ser	arg	cys	phe	glu GAA	thr	his	thr
ser ser	ser	TTC	val	gly	leu CTG	val GTA	TTC
glu	cys	gln	his	leu	ser	his	gln
GAG	TGC	cag	CAT	CTA	TCA	CAT	CAA
leu	91 <i>y</i>	thr	glu	ser	asn	glu	ala
CTG	660	ACT	GAA	TCT	AAC	GAG	GCC
met	leu	glu	tyr	pro	lys	his	ile
ATG	Crc	GAA	TAT		AAA	CAC	ATA
430	400	370	340	310	280	250	220
ala	phe	asn	ser	asn	ile	cys	thr
GCC	TTC	AAC	TCA	AAT	ATA	TGT	ACT
ile	gln	pro	arg	leu	thr	cys	val
ATC	CAG		AGA	CTA	ACA	TGC	GTT
thr	lys	leu	arg	asn	g lu	arg	thr
Acc	AAA	CTT	AGA	AAC	GAA	AGA	ACT
arg	leu	glu	his	arg	cys	gly	lys
AGA	CTA	GAA	CAT		TGC	GGA	AAA
lys	gly	cys	pro	phe	cys	asp	leu
AAA	GGA	TGC		TTT	TGC	GAT	CTG
met	glu	gln	gln	leu	lys	val	ser
ATC	GAA	CAA	cae	TTA	AAA	CTG	AGT
ala ala	tyr	asp	leu	gly	leu	leu	gln
GCA GCC	TAT	GAT	CTT	GGA		CTG	cag
ala	tyr	lys	ala	asp	thr	asp	lys
GCC	TAC	AAA	CCT	GAT	Acc	GAT	MG
thr	leu	gly	val	arg	thr	cys	phe
ACA	TTA	GGA	GTC	AGA	Acc	TGT	TTT
ala	gln	glu	ser	asp	leu	leu	thr
GCA	CAA	GAA		GAT	CTG	CTG	Acc
440	410	380	350	320	290	260	230
ala	asn	glu	val	Phe	glu	gln	1ys
GCC	AAT	GAA	GTA	TTT	gaa	CAG	AAA
thr	ala GCG	glu GAA	ile Att	asn AAC	arg	asp GAT	val CTT
cys	phe	leu	leu	gln	gly	91y	asn
TGT		TTA	CTA	CAA	GGT	666	AAT
cys	leu	gln	arg	phe	gln	glu	phe
TGC	CTC	CAG	AGA	TTT	CAA		TTT
gln	val	lys	val	rer	cys	lys	thr
CAA	GTT	AAA	GTT		TCT	aaa	ACT
leu	ala	tyr	ala	ser	ile	ile	glu
	GCT	TAC	CCT	TCA	ATA	ATC	GAA
ser	tyr	ile	lys	999	ile	met	ile
	TAC	ATC	AAA	AT	ATT	ATG	ATC
glu	thr	gln	gly	glu	his	ser	gln
GAG	ACA	CAG		GAA	CAT	TCC	cag
glu asp GAG GAC	lys AAG	glu GAG	tyr TAC	glu lys GAA AAA	his ala	tyı TAC	240 le gln lys leu val
lys	lys	ser	gln	asn	glu	ile	leu
aaa	aaa		CAG	AAT	GAA	ATA	CTA
450 leu CTA	420 ala GCC	390 gln CAA	360 glu GAG	ile ATC	asn AAT	cys TGT	240 val GTC
450 lys leu haa CTA(1451)	420 lys ala AAA GCC(1361)	390 c gln c caa(1271)	360 n glu 3 GAG(1181)	s asn ile A AAT ATC(1091)	glu asn GAA AAT(1001)	(911)	(821)
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TTCATTCGGTG <u>TGA</u> ACTTTTCTCTCTTTAATTTTAAC <u>TGA</u> TTTAACACTTTTTGTGAATTAATGAAA <u>TGATAA</u> AGACTTTTATGTGAGATTTCC	571 val GTC	541 lys AAG	511 lys AAG	481 cys TGC	451 leu TTG
PICC	cys TGC	pro CCA	phe TTC	cys TGC	ala GCC
CIC	phe TTT	gln CAA	ile ATT	thr	cys TGT
GAA	ala GCT	ile ATA	Dir.	rer	255 718
CTTT	glu GAA	thr ACA	his CAT	ser TCA	glu GAG
PCTC	glu GAG	glu GAG	lys AAG	tyr TAT	gly GGA
TTTA	gly GGA	glu GAA	asp	ala	ala GCG
ATTT	gln	gln	Leu	asn	ala
TAAC	lys AAA	leu CTT	TGC	arg	asp
IGAT	580 leu CTG	550 glu GAG	520 gln CAA	490 arg	460 ile
TTAA(ile ATT	ala GCT	ala GCT	pro	ile ATT
CACT	ser TCA	val GTC	gln	TGC	ile
lll.	lys AAA	ile ATT	gly GGT	phe	gly GGA
GTGA	thr	ala GCA	val GTA	ser	his CAC
ATTA	arg CGT	asp GAT	ala GCG	ser	leu TTA
ATGAJ	ala GCT	phe TTC	leu CTG	leu TTG	Cys
ATO	ala GCT	ser TCA	gln CAA	val	ile MTC
TANK TO THE	leu TTG	gly GGC	thr Acc	val GTG	arg
GACT	gly GGA	leu CTG	met ATG	asp Cat	his CAT
ari di	590 val GTT	560 leu TTG	530 Lys AAG	500 glu GAA	470 glu GAA
TGTG	ter TAA	glu GAG	gln CAA	thr ACA	met ATG
)AGAI	ATT	lys AAA	glu GAG	tyr Tat	thr
JICC	Attactt	roc Toc	phe TTT	val GTC	CCA pro
TTAI	CAGO	TGC CYB	leu CTC	pro pro	val GTA
CACI	ZG Z	cys gln TGC CAA	ile ATT	pro	asn AAC
(GAA)	OAG.	gly GGC	asn AAC	ala GCA	LOS
TAA	AAGA	gln cag	leu CTT	phe TTC	91y
AATA'	CAAA	glu GAA	val GTG	TCT TCT	val
LCTC	ACGA	gln CAG	lys AAG	asp GAT	750 716
CAAA	GTCT	glu GAA	gli CAA	OAC GAC	291 201 201
ttatcacagaaa <u>taa</u> aatatctccaaa (2027)	CAGGGGAAGAGAAAAAAAAGAGTCT (1908)	570 gly gln glu gln glu GGC CAG GAA CAG GAA(1811)	leu ile asn leu val lys gln CTC ATT AAC CTT GTG AAG CAA(1721)	pro pro ala phe ser asp asp CCT CCT GCA TTC TCT GAT GAC(1631)	480 val asn pro gly val gly gln GTA AAC CCT GGT GTT GGC CAG(1541)
2	æ	<u>,</u> E	11)	11)	11)



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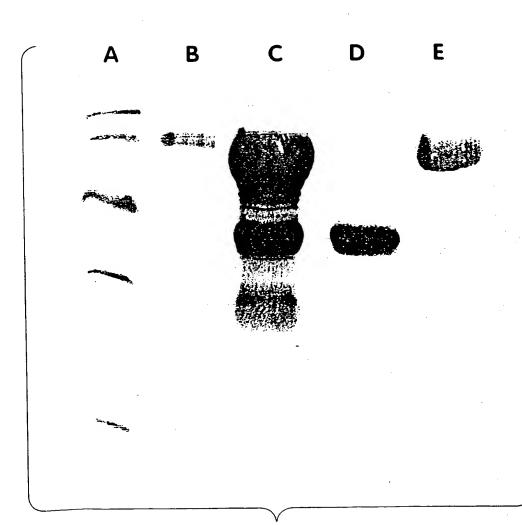


Fig. 2



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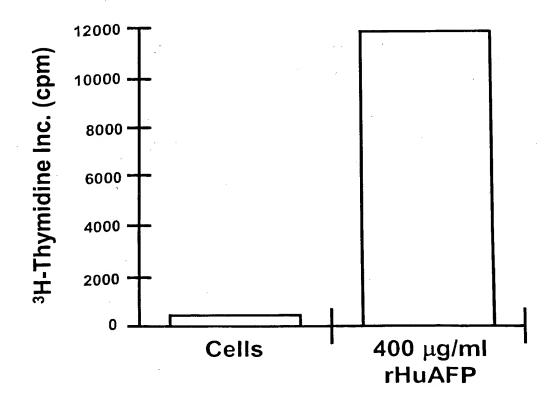


Fig. 3